

## SEQUENCE LISTING

**SEQ ID 1 – *NadA* from strain 2996, with C-terminus deletion**

1AP20 Rec'd 11/13/2006

5 MKHFPSKVLTTAILATFCSGALAAATNDDDVKKAATVAIAAAYNNGQEINGFKAGETIYDIDEDGTITKKDATAA  
DVEADDFKGLGLKKVVTNLTCTVNENKQNVDAKVKAASEIEKLTTKLADTDAALADTDAALDATTNALNKLGE  
NITTFAEETKTNIVKIDEKLEAVADTVDKHAEAFNDIADSLDETNTKADEAVKTANEAKQTAEETKQNVDAKVK  
AAETAAGKAEAAAGTANTAADKAEVAAKVTDIKADIATNKDNIAKKANSADVTTREESDSKFVRIDGLNATTE  
KLDTRLASAEKSIADHDTRLNGLDKTVSDLRKETRQGLAEQAALSGLFQPYNVG

**SEQ ID 2 – *NadA* from strain 2996, with C-terminus deletion and leader peptide processed**

10 ATNDDDVKKAATVAIAAAYNNGQEINGFKAGETIYDIDEDGTITKKDATAADVEADDFKGLGLKKVVTNLTCTV  
NENKQNVDAKVKAASEIEKLTTKLADTDAALADTDAALDATTNALNKLGENITTFAEETKTNIVKIDEKLEAV  
ADTVDKHAEAFNDIADSLDETNTKADEAVKTANEAKQTAEETKQNVDAKVKAETAAGKAEAAAGTANTAADKA  
EVAAKVTDIKADIATNKDNIAKKANSADVTTREESDSKFVRIDGLNATTEKLDTRLASAEKSIADHDTRLNGL  
DKTVSDLRKETRQGLAEQAALSGLFQPYNVG

**SEQ ID 3 – *AG741* from MC58 strain**

15 VAADIGAGLADALTAPLDHKDKGLQSLTLDQSVRKNEKLKLAQAQAEKTYGNGDSLNTGKLKNDKVSRLFDFIRO  
IEVDGQLITLESGEFQVYKQSHSALTAFQTEQIQDSEHSGKMVAKRQFRIGDIAGEHTSFDKLPEGGGRATYRGT  
AFGSDDAGGKLTYYTIDFAAQQNGKIEHLKSPELNVDLAAADIKPDGKRHAVISGSVLYNQAEEKSYSLGIFGG  
KAQEVAGSAEVKTVNGIRHIGLAQK

**SEQ ID 4 – 936 from MC58 strain with leader peptide processed**

20 VSAVIGSAAVGAASAVDRRTTGAQTDDNVMALRIETTARSYLQNNQTKGYTPQISVVGYNRHLHLLGQVATEG  
EKQFVGQIARSEQAAEGVYNYITVASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGIL  
TPEEQAQITQKVSTTVGVQKVITLYQNYVQR

**SEQ ID 5 – 953 from MC58 strain with leader peptide processed**

25 ATYKVDEYHANARFAIDHFNTSTNVGGFYGLTGSVEFDQAKRDGKIDITIPIANLQSGSQHFTDHLKSADIFDA  
AQYPDIFRVSTKFNFGKKLVSDGNLTMHGKTAPVKLKAKEFNCYQSPMEKTEVCGGDFSTTIDRTKWGM DYL  
VNVGMTKSVRIDIQIEAAKQ

**SEQ ID 6 – *AG287* from MC58 strain**

30 SPDVKSADTLSPKPAAPVVSEKETEAKEDAPQAGSQGQGAPSAQGSQDMAAVSEENTGNGGAVTADNPKNEDVA  
QNDMPQNAAGTDSSTPNHTPDNMLAGNMENQATDAGESSQANQPDMANAADMGGDDPSAGGQNAAGNTAAQG  
ANQAGNNQAAGSSDPIPASNPAPANGGSNFRVLDLAVGLIDGPSQNTLTHCKGDCSGNNFLDEEVQLKSEF  
EKLSADADKISNYKKDGKNDKFVGLVADSVQMKGINQYIIFYKPKPTSFAFRRSARSRRSLPAEMPLIPVNQAD  
TLIVDGEAVSLTGHSGNIFAPEGNYRYLTYGAEKLPGGSYALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRP  
YPTRGRFAAKVDFGSKSVGDIIDSGDDLHMGTOQKFAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYSY  
RPTDAEKGFGVFAAGKEQD

35 **SEQ ID 7 – 287-953 hybrid**

10 MASPDVKSADTLSPKPAAPVVSEKETEAKEDAPQAGSQGQGAPSAQGGQDMAAVSEENTGNGGAAATDKPKNEDE  
GAQNDMPQNAADTDSLTPNHTPASNMPAGNMENQAPDAGESEQANQPDMANADGMGGDDPSAGGENAGNTAA  
QGTNQAENNQTAGSQNPASSTNPSATNSGGDFGRNTVGNVVIDGPSQNTLTHCKGDCSGNNFLDEEVQLKS  
EFEKLSADADKISNYKKDGKNDKFVGLVADSVQMKGINQYIIFYKPKPTSFAFRRSARSRRSLPAEMPLI  
PVNQADTLIVDGEAVSLTGHSGNIFAPEGNYRYLTYGAEKLPGGSYALRVQGEPSKGEMLAGTAVYNGEVLHFH  
TENGRPSPSRGRFAAKVDFGSKSVGDIIDSGDGLHMGTOQKFAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEV  
AGKYSYRPTDAEKGFGVFAAGKEQDGGGGGATYKVDEYHANARFAIDHFNTSTNVGGFYGLTGSVEFDQAKR

DGKIDITIPVANLQSGSQHFTDHLKSADIFDAAQYPDIRFVSTKFNFNKGKLVSDGNLTMHGKTAPVKLKA EK  
FNCYQSPMAKTEVCGGDFSTTIDRTKWGVDYLVNVMGTSVRIDIQIEAAKQ\*

**SEQ ID 8 – 936-741 hybrid**

5 MVS AVIGSAAVGA KSAVDRRTTGAQTDDNVMALRIETTARSYL RQNNQTKGYTPQISVVGYNRHL LLLGQVATE  
GEKQFVGQIARSEQAAEGVYNYITVASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGI  
LTPEEQAQITQKVSTTVGVQKVITLYQNYVQRSGGGGVAADIGAGLADALTAPLDHKDKGLQSLTLDQSVRKN  
EKLKLAQAQGAEKTYGNGDSLNTGKLKNDKVS RFD FIRQIEVDGQLITLESGEFQVYKQSHSALTAFQTEQIQDS  
EHSGKMVAKRQFRIGDIAGEHTSFDKLPEGGRATYRGTAFGSDDAGGKLYTIDFAAKQGNKGIEHLKSP ELNV  
DLAAADIKPDGKRHAVISGSVLYNQAEGSYS LGIFGGKAQEVAGSAEVKTVNGIRHIGLA AKQ\*

10 **SEQ ID 9 – linker**

GSGGGG

**SEQ ID 10 – 741 sequence**

15 CSSGGGGVAADIGAGLADALTAPLDHKDKGLQSLTLDQSVRKN EKLKLAQAQGAEKTYGNGDSLNTGKLKNDKVS  
RFD FIRQIEVDGQLITLESGEFQVYKQSHSALTAFQTEQIQDSEHSGKMVAKRQFRIGDIAGEHTSFDKLPEGG  
RATYRGTAFGSDDAGGKLYTIDFAAKQGNKGIEHLKSP ELNVDLAAADIKPDGKRHAVISGSVLYNQAEGSY  
SLGIFGGKAQEVAGSAEVKTVNGIRHIGLA AKQ

**SEQ ID 11 – 741 sequence**

20 CSSGGGGVAADIGAGLADALTAPLDHKDKSLQSLTLDQSVRKN EKLKLAQAQGAEKTYGNGDSLNTGKLKNDKVS  
RFD FIRQIEVDGQLITLESGEFQIYKQDHS AVVALQIEKINNPDKIDSLINQRSFLVSGLGGEHTAFNQLPDGK  
AEYHGKAFSSDDAGGKLYTIDFAAKQGHGKIEHLKTP EQNVELAAAE LKADEKSHAVILGDTRYGSEEKGT YH  
LALFGDRAQEIAGSATVKIGEKVHEIGIAGKQ

**SEQ ID 12 – 741 sequence**

25 CSSGGGGSGGGGVAADIGTGLADALTAPLDHKDKGLKSLTLED SIPQNGTLTLSAQGAEKTFKAGDKD NSLNTG  
KLKNDKISRFDVQKIEVDGQTITLASGEFQIYQNHS AVVALQIEKINNPDKTDSLINQRSFLVSGLGGEHTA  
FNQLPGGKAEYHGKAFSSDDPNGLHYSIDFTKKQGYGRIEHLKTL EQNVELAAAE LKADEKSHAVILGDTRYG  
SEEKGT YHLALFGDRAQEIAGSATVKIGEKVHEIGIAGKQ